

APRIL/MAY 2023

CSMB55 — BIOINFORMATICS

Time : Three hours

Maximum : 75 marks

SECTION A — (10 × 2 = 20 marks)

Answer ALL questions.

1. Write expansion EMBL
2. Write expansion DDBJ
3. Explain BLAST
4. What is BLAST technique?
5. What is genomics used for?
6. What are the types of genomics?
7. What are the two goals of Human Genome Project?
8. What three additional organisms were studied during the human genome Project?
9. Define Two-dimensional gel electrophoresis
10. MALDI-TOF

SECTION B — (5 × 5 = 25 marks)

Answer ALL questions.

11. (a) Discuss progressive alignment method?

Or

- (b) Write short note on Phylogenetic tree?

12. (a) Explain the Chou-Fasman method for protein secondary structure prediction?

Or

- (b) Outline the levels of organization of protein structure?

13. (a) Mention the techniques are used in comparative genomics?

Or

- (b) Explain the applications of comparative genomics?

14. (a) Explain specific goal of HGP?

Or

- (b) What are model organisms?

15. (a) Explain the application of Mass Spectroscopy in proteomics?

Or

- (b) Explain 2D SDS-PAGE?

SECTION C — (3 × 10 = 30 marks)

Answer any THREE questions.

16. Discuss in detail any one algorithm for multiple sequence alignment?

17. Explain FASTA algorithm in detail with recommended steps for similarity searching?

18. What is sanger sequencing and explain it?

19. Discuss in detail Human genome project?

20. Explain high throughput methods of proteomics?